





## JOURNAL

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## COMMENT

On Nov 14, 1999 this sequence version replaced 31-172146  
Sequence updated (05-Nov-1999)

## FEATURES

## SOURCE

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/tissue\_type="testis"

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/gene="hAcpw"

85..870

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/product="aquaporin 8"

/protein\_id="AA4442.1"

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1309

/gene="hAcpw"

/note="32 a nucleotides"

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1

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[illegible]

ACCESSION: RC010987  
 VERSION: 1  
 DEFINITION: Mouse mammary gland cDNA library.  
 ACCESSION: M60424-4850, mRNA, complete cds.  
 ACCESSION: BC010982.1 GI:15012144  
 VERSION: 1  
 DEFINITION: Mus musculus house mouse.  
 ORGANISM: Mus musculus  
 TISSUE: Mammary gland  
 DEVELOPMENTAL STAGE: Embryo  
 GENE: Cdkn1a  
 REFERENCE: 1. (bases 1 to 1455)  
 SOURCE: EMBL  
 COMMENT: Direct Submission  
 SUBMITTER: National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A01, Bethesda, MD 20892-2840, USA  
 NIH MGC Project URL: <http://mgc.nhl.nih.gov>  
 CONTACT: MGC help desk  
 EMAIL: [cgpps@mail.nih.gov](mailto:cgpps@mail.nih.gov)  
 TISSUE Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Analyzed by: The I.M.A.G.E. Consortium (www.cdna.org)  
 DNA Sequencing by: Institute for Systems Biology  
 URL: <http://www.systemsbio.org>  
 CONTACT: amanda@systemsbio.org

Amel Madan, Jessica Ekby, Erin Holton, Mark Kottmann, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whitting

SCIENTIFIC  
SOURCES

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source
1. 1456
/feature "name" "scutulus"
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99. 1881
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22

BASE COPY  
ORIGIN

Query Match: 38.4%; Score 520.6; DB 10; Length 145;  
Best Local Similarity 74.7%; Prod. No. 2.8e 105;  
Matches 666; Conservative 8; Mismatches 224; Indels 17; Gaps 17;

[illegible]

[illegible][illegible]

24762		gap of unknown length	*
24763	24762-24763	1852 bp in length	*
24764	24763-24764	unknown length	*
24765	24764-24765	1914 bp in length	*
24766	24765-24766	gap of unknown length	*

Accession	Gene	Length (bp)	Gap of unknown length
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*	8679	341	of unknown length
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Accession	Strain	Sex	Age	Length	Weight	Length of 1st segment	Length of 2nd segment	Length of 3rd segment	Length of 4th segment	Length of 5th segment	Length of 6th segment	Length of 7th segment	Length of 8th segment	Length of 9th segment	Length of 10th segment	Length of 11th segment	Length of 12th segment	Length of 13th segment	Length of 14th segment	Length of 15th segment	Length of 16th segment	Length of 17th segment	Length of 18th segment	Length of 19th segment	Length of 20th segment	Length of 21st segment	Length of 22nd segment	Length of 23rd segment	Length of 24th segment	Length of 25th segment	Length of 26th segment	Length of 27th segment	Length of 28th segment	Length of 29th segment	Length of 30th segment	Length of 31st segment	Length of 32nd segment	Length of 33rd segment	Length of 34th segment	Length of 35th segment	Length of 36th segment	Length of 37th segment	Length of 38th segment	Length of 39th segment	Length of 40th segment	Length of 41st segment	Length of 42nd segment	Length of 43rd segment	Length of 44th segment	Length of 45th segment	Length of 46th segment	Length of 47th segment	Length of 48th segment	Length of 49th segment	Length of 50th segment	Length of 51st segment	Length of 52nd segment	Length of 53rd segment	Length of 54th segment	Length of 55th segment	Length of 56th segment	Length of 57th segment	Length of 58th segment	Length of 59th segment	Length of 60th segment	Length of 61st segment	Length of 62nd segment	Length of 63rd segment	Length of 64th segment	Length of 65th segment	Length of 66th segment	Length of 67th segment	Length of 68th segment	Length of 69th segment	Length of 70th segment	Length of 71st segment	Length of 72nd segment	Length of 73rd segment	Length of 74th segment	Length of 75th segment	Length of 76th segment	Length of 77th segment	Length of 78th segment	Length of 79th segment	Length of 80th segment	Length of 81st segment	Length of 82nd segment	Length of 83rd segment	Length of 84th segment	Length of 85th segment	Length of 86th segment	Length of 87th segment	Length of 88th segment	Length of 89th segment	Length of 90th segment	Length of 91st segment	Length of 92nd segment	Length of 93rd segment	Length of 94th segment	Length of 95th segment	Length of 96th segment	Length of 97th segment	Length of 98th segment	Length of 99th segment	Length of 100th segment																																																																																																																													
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43646	Contig of 5382 bp in length
43629	part of unknown length
43787	part of unknown length
43728	Contig of 4565 bp in length
48097	part of unknown length

[illegible]

Accession	Gene	Length (bp)
U00001	16S rRNA	1600
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U00077	23S rRNA	2300
U00078	5S rRNA	120
U00079	16S rRNA	1600
U00080	23S rRNA	2300
U00081	5S rRNA	120
U00082	16S rRNA	1600
U00083	23S rRNA	2300
U00084	5S rRNA	120
U00085	16S rRNA	1600
U00086	23S rRNA	2300
U00087	5S rRNA	120
U00088	16S rRNA	1600
U00089	23S rRNA	2300
U00090	5S rRNA	120
U00091	16S rRNA	1600
U00092	23S rRNA	2300
U00093	5S rRNA	120
U00094	16S rRNA	1600
U00095	23S rRNA	2300
U00096	5S rRNA	120
U00097	16S rRNA	1600
U00098	23S rRNA	2300
U00099	5S rRNA	120
U00100	16S rRNA	1600

id	gap	length
00932	117607	Gap of unknown length
117687	Gap of unknown length	
117688	117687	Gap of unknown length
117689	144002	Gap of unknown length
117690	504417	Gap of unknown length

•		known length
•	7698	247 bp in length
•	7699	1011 bp in length
•	7700	1011 bp in length
•	7701	340 bp in length
•	7702	contig of 6297 bp in length

DATE \_\_\_\_\_  
PAGE NO \_\_\_\_\_  
COURSE \_\_\_\_\_  
ROLL NO \_\_\_\_\_  
NAME OF THE ORGANISM- "Homo sapiens"











\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.biorb.com/edu/docs/genbank\\_draft\\_data.html](http://www.biorb.com/edu/docs/genbank_draft_data.html))  
 \* NOTE: This is a 'working draft'. Currently  
 \* consists of 66 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

52328	52427:	gap of unknown length
52428	52424:	contig of 3497 bp in length
52429	52424:	gap of unknown length
53225	53278:	contig of 1354 bp in length
53279	53378:	gap of unknown length
53379	53724:	contig of 2446 bp in length
53725	53724:	gap of unknown length
53726	53661:	contig of 1747 bp in length
53727	53661:	gap of unknown length
53728	53510:	contig of 1242 bp in length
53729	53510:	gap of unknown length
53730	53952:	contig of 2342 bp in length
53953	54052:	gap of unknown length
54054	57489:	contig of 3437 bp in length
54055	57589:	gap of unknown length
54056	57050:	contig of 3461 bp in length
54057	57150:	gap of unknown length
54058	574048:	contig of 2898 bp in length
54059	574148:	gap of unknown length
54060	577038:	contig of 2890 bp in length
54061	577138:	gap of unknown length
54062	579459:	contig of 2321 bp in length
54063	579559:	gap of unknown length
54064	82098:	contig of 3139 bp in length
54065	82758:	gap of unknown length
54066	85025:	contig of 2227 bp in length
54067	85125:	gap of unknown length
54068	86657:	contig of 3532 bp in length
54069	86757:	gap of unknown length
54070	93164:	contig of 4407 bp in length
54071	93264:	gap of unknown length
54072	95265:	contig of 2646 bp in length
54073	95266:	gap of unknown length
54074	98791:	contig of 2831 bp in length
54075	98891:	gap of unknown length
54076	103852:	contig of 5001 bp in length
54077	103992:	gap of unknown length
54078	107044:	contig of 3052 bp in length
54079	107444:	gap of unknown length
54080	111412:	contig of 4268 bp in length
54081	111512:	gap of unknown length
54082	115079:	contig of 3563 bp in length
54083	115175:	gap of unknown length
54084	118661:	contig of 3486 bp in length

[illegible]

Search completed: January 12, 2003, 01:31:45  
Job time : 2906.18 secs

Genome version 5.1.3  
Copyright 1999-2000 Washington

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Copyright 1999-2000 Washington

Genome version 5.1.3  
Copyright 1999-2000 Washington

Result No.	Score	Query	Length	DB	ID	Description
1	1354	100.0	1354	21	AA589924	CDNA sequence of a
2	1313.4	99.6	1313	21	AA589924	Human colon cancer
3	1213.4	99.6	1410	22	AA589924	Human colon cancer
4	1173.4	99.6	1410	22	AA589924	Human colon cancer
5	1173.4	99.6	1410	22	AA589924	Human colon cancer
6	1173.4	99.6	1410	22	AA589924	Human colon cancer
7	1173.4	99.6	1410	22	AA589924	Human colon cancer
8	1173.4	99.6	1410	22	AA589924	Human colon cancer
9	1173.4	99.6	1410	22	AA589924	Human colon cancer

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

Listing first 45 summaries

Listing first 45 summaries

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# ALIGNMENTS

## RESULT 1

AA589924

AA589924

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Novel human diatom









[illegible][illegible]

RESULT 6  
ABK13/63  
ABK12764 standard: DNA: 1448 BP.



XX  
PD 13-SEP-2001.  
XX  
OF MAR-2001; 2001WC-US07787.  
XX  
OF-MAR-2000; 2000US-0184609.  
XX  
(CHIR ) CHIRON CORP.  
XX {HYSEQ } HYSEQ INC.

XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth Kliner JJ,  
XX Reinhard C, Raczko F, Kennedy GC, Pot D, Fassam A, Lamson G;  
XX Dimanche P, Chwyzgowy P, Dickson M, Dimanche S, Labat I;  
XX Leskowitz B, Vilar L, Garcia V, Lopez WL, Strache Chain B;  
PI

XX WPI; 2001-SAP777/58.  
XX  
XX New polynucleotides and polypeptides useful for diagnosis and  
XX treatment of breast, lung and colon cancer  
XX  
XX Claim 1; Page 1162; 119pp; English.

XX The invention relates to new polym nucleotides and polypeptides, useful for  
XX diagnosing colorectal cancer. Four and seven amino acid sequences  
XX can be used in detecting differentially expressed genes correlated with a  
XX cancerous state of a mammalian cell, comprising determining at least one  
XX differentially expressed gene product in a test sample derived from a  
XX cell suspected of being cancerous. They can also be used to inhibit  
XX tumor growth by modulating expression of a gene product. AAS3694  
XX Nucleotide represent novel human diagnostic and therapeutic coding  
XX sequences of the invention.

XX Sequence 317 BP; 49 A; 98 C; 96 G; 73 T; 1 other;

Query Match            23.1%; Score 312.8; DB 22; Length 417;  
Best local similarity    99.4%; Pred No. 8, 16 / 72;  
Matches 314; Conservative    0; Mismatches    2; Indels    0; Gaps    0;

QY 741 CGGGCCCTGTGTTTGCGAGGCTTGAATACCAAAACAAGAATTTCGCACGCCGCGTTGG 790  
DB 1 GGCGCCCCGTGTCGTGAGAGGCTCATCATAAACCACCCCACCTTTTTCAGTAATGCGGTATRG 60

QY 791 CCAGCACAGCAACTTCACATGATATACAGTAGTATGACCACTCTCTCTCTCTCTCTCTCTCT 850  
DB 61 CCACACACCGAACATTCACATGATATACAGTAGTATGACCACTCTCTCTCTCTCTCTCTCTCT 120

QY 851 TTGGACAGCTCAAITAGTGTGCTTCATTGAGATGAGAAAGAACCCCTCCTATCTGTAAGGCTT 910  
DB 121 TTGACAGCTCATTAGTGCTTCTTATTGAGATGAGAAAGAACCCCTCCTCCTCCTCCTCCT 180

QY 911 GTTMAAGAGAGAGTCT 970  
DB 181 GGTGAAGACAGAGCTCTGTGGGATTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

QY 971 ACAGACAGACAG 1030  
DB 241 ACTCAGACAG 400

QY 1031 CTGCTTCACAGCTGCTTG 1046  
DB 301 CTGCTTCACAGCTGCTTG 416

RESULT 9  
AAS9303  
ID AAS49303 standard; cDNA; 318 BP.  
XX  
XX AAS39303;  
XX  
XX 17-DEC-2001 (first entry)  
XX Novel human diagnostic and therapeutic gene #2361.  
DE XX



RESULT 12	
ID AB199474	# standard, cDNA; 449 bp.
XX AC AB199474;	
XX AD AB199474;	
DT 07-MAR-2002	(first entry)
XX SE Mouse ischaemic condition induced RNA response SEQ ID NO:448.	
XX KW Mouse; ischemia; compressive ischaemia; exclusive ischaemia; vascular ischaemia; ischaemic condition; ischaemic disease; ms.	
XX OS Mus musculus.	
XX WO200188188 A2.	
XX PD 22 NOV 2001.	
XX FP 18 MAY 2001; 2001WO-IP04192.	
XX PR 18-MAY-2000; 2000JP-0145977.	
FA {UTM : UNIV MIHON SCHOOL MEDICAL RESEARCH,	
P1 Ishikawa K., Asai S., Takahashi Y., Nagata T., Ishii Y.	
DR WPI; 2002-09463/04.	
XX EX Examining the ischaemic condition ( <i>c.g.</i> occlusive ischaemia) by measuring expression levels of particular genes defined in the specification or by automating the expression profile of a gene group comprising these genes -	
PS Claim 2; Page 1180; 2690pp; English.	
CC The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition ( <i>c.g.</i> compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199474 to AB199919), encoding the protein sequences in AB57626 to AB57634, or by determining the expression profile of a gene group comprising these genes. The used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB199919 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.	
SQ Sequence 435 bp; 85 A, 107 C, 145 G; 112 T; 0 other;	
Query Match	10.5% Score 223.4; DB 23; Length 449;
Best Local Similarity	79.8%; Pred. No. In 48;
Nucleus 20n, Conservative	2; Mismatch 50; Gap 0; Gaps
QY 463 GCTGGGAGATGTTTGTGTCACCGAAAGCAGCAAGGCATGAGAGATTCTTG 542       	
DQ 81 GTTAGGAGAATCATAGGGGCTGCCCTGTAAGACTGATGAACAAGAAAATT TG 189       	
QY 543 GAATGATCTGGGCCCCCTTTGTGTGACAGTCACGACATACGACACAGGACATTAAGAGCTTT 662       	
DQ 140 GATATGATCGGGGAGGCTTTCGATATGCTAATGCTCACGATGAGGATAAGATGATGAT 199       	
QY 603 GGATGAGAT 662       	
DQ 209 GGGATAGAGATCATTTGTACCAATGCTTGTGATGTGGATGTTGATATGGATGCTCTAA 259       	
QY 663 TAGAT 722       	
DQ 90 TGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419       	

[illegible]





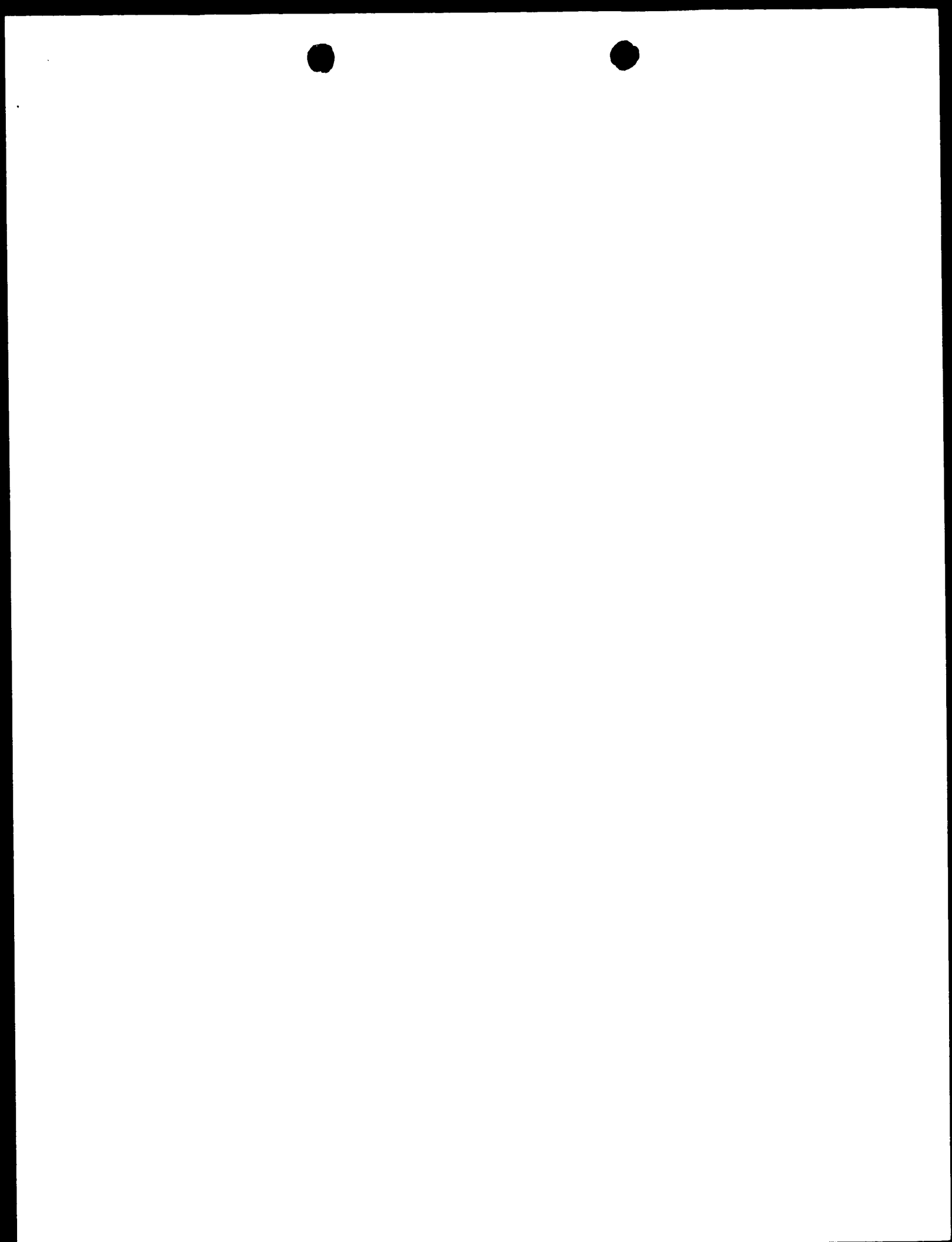


Mon Jan 13 09:24:13 2003

us-09-864-711-8.rng

Page 13

Job time : 206.731 secs



[illegible][illegible]





































US 09 887 576 804  
 : Sequence 804, Application US/09887576  
 : Parent No. US20020144047A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Budworth, P.  
 : APPLICANT: Brown, D.  
 : APPLICANT: Chang, H.  
 : APPLICANT: Zhu, T.  
 : APPLICANT: Han, B.  
 : APPLICANT: Wang, X.  
 : APPLICANT: Cooper, Bret  
 : TITLE OF INVENTION: Promoters for regulation of plant expression  
 : FILE REFERENCE: 1360 001051  
 : CURRENT APPLICATION NUMBER: US/09887576  
 : CURRENT FILING DATE: 2001-06-25  
 : PRIOR APPLICATION NUMBER: US 60/213,848  
 : PRIOR FILING DATE: 2000-06-23  
 : PRIOR APPLICATION NUMBER: US 60/214,987  
 : PRIOR FILING DATE: 2000-06-23  
 : PRIOR APPLICATION NUMBER: US 60/258,692  
 : PRIOR FILING DATE: 2000-12-29  
 : NUMBER OF SEQ ID NOS: 975  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 804  
 : LENGTH: 560  
 : TYPE: DNA  
 : ORGANISM: Oryza sativa  
 : US 09 887-576-804

Query Match 5.8%; Score 72.2; db 1; Length 560;  
 Best Local Similarity 50.0%; Pred. No. 1.5e-12;  
 Matches 219; Conservative 0; Mismatches 221; Indels 15; Gaps 11

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41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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US 09 887-576-805  
 : Sequence 805, Application US/09887576  
 : Parent No. US20020144047A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Budworth, P.  
 : APPLICANT: Brown, D.  
 : APPLICANT: Chang, H.  
 : APPLICANT: Zhu, T.  
 : APPLICANT: Han, B.  
 : APPLICANT: Wang, X.  
 : APPLICANT: Cooper, Bret  
 : TITLE OF INVENTION: Promoters for regulation of plant expression  
 : FILE REFERENCE: 1360 001051  
 : CURRENT APPLICATION NUMBER: US/09887576  
 : CURRENT FILING DATE: 2001-06-25  
 : PRIOR APPLICATION NUMBER: US 60/213,848  
 : PRIOR FILING DATE: 2000-06-23  
 : PRIOR APPLICATION NUMBER: US 60/214,987  
 : PRIOR FILING DATE: 2000-06-23  
 : PRIOR APPLICATION NUMBER: US 60/258,692  
 : PRIOR FILING DATE: 2000-12-29  
 : NUMBER OF SEQ ID NOS: 875  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 805  
 : LENGTH: 765  
 : TYPE: DNA  
 : ORGANISM: Oryza sativa  
 : US 09 887-576-805

Query Match 5.7%; Score 76.0; db 10; Length 765;  
 Best Local Similarity 49.9%; Pred. No. 9.4e-12;  
 Matches 233; Conservative 0; Mismatches 219; Indels 15; Gaps 17

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41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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RESULT 14  
 : Sequence 842A-2613  
 : Sequence 2633, Application US/09918842A  
 : Parent No. US20020144047A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Harper, Jeff  
 : APPLICANT: Kreps, Joel















[illegible][illegible]



[illegible][illegible]











